

433-451 Computational Genomics

Credit Points:	12.500
Level:	Undergraduate
Dates & Locations:	2008, This subject commences in the following study period/s: Semester 1, - Taught on campus.
Time Commitment:	Contact Hours: Twenty-Four hours of lectures, 12 hours of laboratory work Total Time Commitment: Not available
Prerequisites:	Two semesters of programming experience or equivalent.
Corequisites:	None
Recommended Background Knowledge:	None
Non Allowed Subjects:	None
Core Participation Requirements:	<p><p>For the purposes of considering request for Reasonable Adjustments under the Disability Standards for Education (Cwth 2005), and Student Support and Engagement Policy, academic requirements for this subject are articulated in the Subject Overview, Learning Outcomes, Assessment and Generic Skills sections of this entry.</p> <p><p>It is University policy to take all reasonable steps to minimise the impact of disability upon academic study, and reasonable adjustments will be made to enhance a student's participation in the University's programs. Students who feel their disability may impact on meeting the requirements of this subject are encouraged to discuss this matter with a Faculty Student Adviser and Student Equity and Disability Support: http://services.unimelb.edu.au/disability</p></p> </p>
Coordinator:	Dr L Stern
Subject Overview:	Topics covered include: computational issues in physical mapping of DNA, in genome annotation, and in analysing gene expression data; motif extraction; methods for determining phylogenetic trees; RNA structure determination; and protein structure determination.
Assessment:	One 3-hour examination (70%) and assignments of up to 2,500 words equivalent (30%). Both project work and examination component of assessment must be completed satisfactorily to pass the subject.
Prescribed Texts:	None
Breadth Options:	This subject is not available as a breadth subject.
Fees Information:	Subject EFTSL, Level, Discipline & Census Date, http://enrolment.unimelb.edu.au/fees
Generic Skills:	<p>On successful completion, students should be familiar with:</p> <ul style="list-style-type: none"> # The computational methods used for constructing, annotating, and comparing, DNA gene sequences; # The underlying theory behind these methods; # Describe current research issues in bioinformatics.
Related Course(s):	Bachelor of Engineering (Biomedical)Bioinformatics